REMARKS / ARGUMENTS

Objections to the Specification

The specification was objected to under 37 CFR 1.821(d) for failing to comply with the requirements for disclosure of nucleotide and/or amino acid sequences. It was noted that some sequence identifiers were missing or did not correspond to the appropriate sequences. Applicants have amended the claims herein to correct the sequence identifiers.

The Examiner has also objected that the dependency of several claims appears to be incorrect. Upon final election of the claims to be prosecuted, Applicants intend to correct any inconsistencies in the claims resulting from incorrect dependency.

Submission of Substitute Sequence Lisiting

Applicants hereby submit a substitute paper copy and computer readable form (CRF)of the "Sequence Listing" for the purpose of making minor corrections in response to the Examiner's comments in paragraph 3A of the present Office Action.

The Claims

Pending Claims 1-42 are directed to CRP1 and B7RP1 polypeptides, nucleic acids encoding the polypeptides, vector, host cells, method of production of the polypeptides, antibodies which bind the polypeptides, and various methods of using the polypeptides and agonists and antagonists thereof. Four specific amino acid sequences are referenced in the claims. These sequences correspond to murine CRP1 (Figure 1A and SEQ ID NO:2), murine B7RP1 (Figure 2A and SEQ ID NO:7), human B7RP1 up to and including amino acid residue 288 (Figure 3A and SEQ ID NO:12) and human B7RP1 up to and including amino acid residue 302 (Figure 12A and SEQ ID NO:17). The corresponding nucleotide sequences are also referenced in the claims. In addition, the claims encompass related CRP1 and B7RP1 sequences such as mature sequences, fragments, orthologs, allelic variants, alternative splice variants and others.

The Restriction Requirement

The Examiner has required restriction of the currently pending claims into 81 restriction groups. Without listing each individual restriction group and the corresponding subject matter, Applicants summarize the restriction requirement as follows:

I-IV (Claims 1-7) correspond to isolated nucleotide sequences, vectors, host cells and methods of producing the polypeptide.

V-VIII (Claims 8-12 and 19-23) correspond to polypeptides, fragments and compositions thereof.

IX-XII (Claims 13-18) correspond to an antibody or fragment thereof.

XIII-XVI (Claim 24) correspond to a method of treating or preventing a T cell disorder.

XVII-XX (Claim 25) correspond to a method of diagnosing a T cell disorder.

XXI-XXIV (Claims 26 and 27) correspond to a method of identifying a test molecule that binds to a polypeptide.

XXV-XXVIII (Claim28) correspond to a method of regulating T cell activation by administering a nucleic acid.

XXIX-XXXII (Claim 29) correspond to a transgenic non-human mammal.

XXXIII-XLVI (Claims 30-38) correspond to a method of decreasing IgE production.

XLVII-LXXXI (Claims 39-42) correspond to a method of enhancing an immune response.

The Examiner alleges that several structurally distinct polypeptides are disclosed in the specification and that each of the structurally distinct polypeptides are subject to restriction because they do not share "a substantial structural feature essential to a common utility" (citing MPEP 803.02 relating to restriction practice for Markush type claims). As a consequence, the claims have been divided into 81 restriction groups, each one characterized by one of the specific nucleotide and/or amino acid sequences recited in the claims. Applicants traverse the restriction requirement for the reasons set forth below.

Applicants maintain it would not place an undue burden on the Examiner to search and examine the specific nucleotide and/or amino acid sequences disclosed in the application. The number of specific sequences is sufficiently few and the relatedness of the sequences is such that the burden would not be undue. For example, SEQ ID NO:17 refers to an amino acid sequence which is 14 amino acids longer than that disclosed in SEQ ID NO:12. Consequently, any search for SEQ ID NO:12 and SEQ ID NO:17 would be co-extensive and not be an undue burden on the Examiner. Moreover, SEQ ID NO:7 depicts the amino acid sequence of murine B7RP1 while SEQ ID NO:12 and SEQ ID NO:17 depict human B7RP1. These polypeptides are related structurally and share a common utility of stimulating T cell function. Applicants maintain it would not place an undue burden on the Examiner to search species variants of a B7RP1 polypeptide.

The Examiner also fails to consider the provisions of Section 803.04 of the MPEP which permits the examination of up to ten independent and distinct sequences in a single application. This section states in part the following:

> It has been determined that normally ten sequences constitute a reasonable number for examination purposes. Accordingly, in most cases, up to ten independent and distinct nucleotide sequences will be examined in a single application without restriction. [Applicants' emphasis]. In addition to the specifically selected sequences, those sequences which are patentably indistinct from the selected sequences will also be examined.

In view of this, it is appropriate under current Office practice for the Examiner to rejoin those claims directed to different specific sequences disclosed in the application.

Applicants request that the restriction requirement be withdrawn in it entirety or, at the very least, that it be withdrawn with respect to the specifically disclosed sequences.

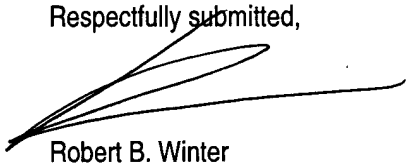
Responsive to the restriction requirement, Applicants provisionally elect Group XXXVI corresponding to Claims 30-34 and 36, drawn to a method of suppressing an immune response/IgE production by administering an antagonist of a B7RP1 polypeptide of SEQ ID NO:17. Applicants traverse the restriction requirement for the reasons set forth above.

In view of Applicants' election of Group XXXVI, the Examiner has required election of a single disclosed species of each recited antagonist having adequate support in the specification under 35 U.S.C. 112. Applicants elect an antibody as a species to which the claims would be restricted if no generic claim were held allowable. The elected species is disclosed in the application at p. 66, lines 12-15. Among currently pending claims, Claim 34 would be readable upon the elected species.

CONCLUSION

It is requested that the restriction requirement be withdrawn with respect to the instantly disclosed nucleotide and amino acid sequences and all sequences be examined on their merits.

Respectfully submitted,



Robert B. Winter
Attorney/Agent for Applicant(s)
Registration No.: 34,458
Phone: (805) 447-2425
Date: MAY 17, 2002

Please send all future correspondence to:

U.S. Patent Operations/RBW
Dept. 4300, M/S 27-4-A
AMGEN INC.
One Amgen Center Drive
Thousand Oaks, California 91320-1799

VERSION WITH MARKINGS TO SHOW CHANGES MADE

Figure 1. A) (SEQ ID NOS: 1 & 2) DNA and amino acid sequence murine CRP1 (mCRP1). Predicted signal sequence of CRP1 is underlined at the amino-terminus and the experimentally determined pro-peptide cleavage site is indicated by an asterisk. Predicted transmembrane sequence is underlined toward the carboxy-terminus. B) (SEQ ID NOS: 3, 4 & 5) ...

Figure 2. A) (SEQ ID NOS: 6 & 7) DNA and amino acid sequence of murine B7RP1 (mB7RP1). Predicted signal sequence of B7RP1 is underlined at the amino-terminus and the experimentally determined pro-peptide cleavage site is indicated by an asterisk. Predicted transmembrane sequence is underlined toward the carboxy-terminus. B) (SEQ ID NOS: 8, 9 & 10) Amino acid alignment of B7RP1 protein sequence (mB7RP1) with murine CD80 (mCD80).

Figure 3. A) (SEQ ID NOS: 11 & 12) Structure and sequence of the protein coding region of the putative human B7RP1 (hB7RP1). Predicted signal sequence of hB7RP1 is underlined at the amino-terminus. Predicted signal peptide cleavage sites are marked by asterisks. Predicted transmembrane sequence is underlined toward the carboxy-terminus. B) (SEQ ID NOS: 13, 14 & 15) Amino acid alignment of the putative mature hB7RP1 protein with the mature murine B7RP1 (mB7RP1) protein.

Figure 12. A) (SEQ ID NOS: 16 & 17) Structure and sequence of the protein coding region of human B7RP1 (hB7RP1). Predicted signal sequence of hB7RP1 is underlined at the amino-terminus. Predicted signal peptide cleavage sites are marked by asterisks. Predicted transmembrane sequence is underlined toward the carboxy-terminus. B) (SEQ ID NOS: 18, 19 & 20) Amino acid alignment of the putative mature hB7RP1 protein with the mature murine B7RP1 (mB7RP1) protein.

Figure 13. A) (SEQ ID NOS: 21 & 22) Structure and sequence of the protein coding region of human CRP1 (hCRP1). Predicted signal sequence of hCRP1 is underlined at the amino-terminus. Predicted signal peptide cleavage sites are marked by asterisks. Predicted transmembrane sequence is underlined toward the carboxy-terminus. B) (SEQ ID NOS: 23 & 24) Amino acid alignment of the hCRP1 protein with the murine CRP1 (mB7RP1) protein.

2. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

a) the nucleotide sequence as set forth in Figure 2A (SEQ ID NO: [11] 6) or Figure 3A (SEQ ID NO: [6] 11) or Figure 12A (SEQ ID NO: 16);

b) the nucleotide sequence encoding the polypeptide as set forth in Figure 2A (SEQ ID NO: 6) from residues 1-322 or from residues 47-322, or as set forth in Figure 3A (SEQ ID NO: 11) from residues 1-288 or from residues 19-288, 20-288, 21-288, 22-288, 24-288, or 28-288 or as set forth in Figure 12A (SEQ ID NO: 16) from residues 1-302, or from residues 19-302, 20-302, 21-302, 22-302, 24-302 or 28-302;

c) a nucleotide sequence encoding a polypeptide that is at least about 70 percent identical to the polypeptide as set forth in Figure 2A (SEQ ID NO: 6) or Figure 3A (SEQ ID NO: 11) or Figure 12A (SEQ ID NO: 6);

d) a naturally occurring allelic variant or alternate splice variant of any of (a), (b) or (c);

e) a nucleotide sequence complementary to any of (a), (b) or (c);

f) a nucleotide sequence of (b),(c) or (d) encoding a polypeptide fragment of at least about 25, 50, 75, 100, or greater than 100 amino acid residues;

g) a nucleotide sequence of (a), (b) or (c) comprising a fragment of at least about 10, 15, 20, 25, 50, 75, 100, or greater than 100 nucleotides; and

h) a nucleotide sequence which hybridizes under stringent conditions to any of (a)-(g).